

[illegible]

FIG. 1A



1 CGATCCGCGTGGCAGATGCATGTCTCTTTGCCAGCCAAGTCATGTTTTCTTGCGGGAACGCTTGGCTGGACTATTGTGGGCTCGTGTGCGCTTGGCCCTGCAAA  
-31 K D V S L C P A K C S F W R I F L L G S V W L D Y V G S V L A C P A N +1

121 TGTCTCTGCAGCAGACTGCAGATCAAATTGCGCGCGCGGAGAAGATGGGAAGGAGATTCAGGGAAAGCAGCATTCAGGAATCGAATCATCACGAG  
S C V C S K T E I N C R R P D D G N L F P L L E G Q D S G N S N G N A N I [N I T D]

241 ATCTOAGCGAATAATCATTCCATACAGATAGAGAACCTGGCGAGTCTTCACAGCTCAACGGCGTGACAATGGAGCTCTACACGGAGTTCMAAAGCTCACCATCAAGAACTCAGAGATT  
45 I S R [N I T S] I H I E N W R S L H T L N A V D M E L Y T G L Q K L T I K N S G L

361 CGAGCAATTGAGCCGAGAGCTTTGCCAAAGCCCCCATTTGCGTTATATAACCTCTCAAGTAACGGCTCACACACTTCTGTGGAGCTTTCCAGACCTCGAGTTCCTGGGAATT  
85 R S I Q P R A F A K N P H L R Y I [N L S S] N R L T T T L S W Q L F Q T L S L R E L

481 CAGTTGGAGCAGAACTTTTCACTGAGCTGTGACATCCCGTGATGCCAGCTCTGGACAGCAGCGGAGCGCAAGCTCAACAGCCAGAACCTCTACTGCAATCAATCTGATGCCTC  
125 Q L E Q N F F [N C S G] D I R W H Q L W Q E Q G E A K L N S Q N L Y C I N A D G S

601 CAGCTTCTCTTTCGGCATCAACATCAGTCACTGTGACCTTCTGAGATCAGCGTGAGCGCAGCTCAACTGACCGTAGCAGAGGTGACAAATGCTGTATTACATCTCCMATGGCTCTGGA  
165 Q L P L F R H [N I S Q] C D L P E I S V S H V [N L T V] R E G D N A V I T C [N G S G]

721 TCACCCTTCTCATGTGCGATGATGACTGCTGCGCTGCAGTCATCAACTCACAGAGCAATCTGAJCTGGAGCAATGTTTCATGCCATCAACTTGAAGCTGTGTAATGTCAGCT  
205 S P L P D V D W I V T G L Q S I N T H Q T N L [N W T N] V H A I [N L T L] V [N V T S]

841 GAGACAAATGGCTTCAACCTCAGCTGCATTCGAGAGAAGCTGTGCGCATGAGCAATGCGAGTTTGGCCCTCACTGTCTACTATCCCGCAGCTGTGTGAGCTTGGAGGAGCCTCAGCTG  
245 E D N G F T L T C I A E N V V G H S [N A S V] A L T V Y Y P P R V V S L E E P E L

961 CGCTGCGAGCACTOCAATCGAGTTTGTGTGGCTGGCAAGCCCACCAAGCTGCACTGGCTGCACAAATGGCGAGCTCTGCGGAGTC CAAGATCATCATGTGGAATACTACCAAG  
285 R L E H C I E P V V R G N P P P T L H W L H N G O P L R E S K I I H V E Y Y Q E

1081 GGAGAGATTTGCAAGGCTGCTCTTCAAGAGCCCACTACACAAATGGCAAACTATACCTCATTTGCCAAAACCCACTGGCGCAGCGCAACCAAGCAGCAATCAATGGCAGCTTC  
325 G E I S E G C L L F N K P T H Y N N G [H Y T L] I A K N P L G T A [N Q T I] N G H F

1201 CTCAGGAGCGCTTTCAGAGAGCAGCGATTAATTTATCTTGTTCAGAGTAGTC CCAGAGCTCTATACACTGTGACCCACAAACCAAGAGAGACACTTTTTCGGGTATCCATAGCA  
365 L K E P F P {E S T D N F I L F} D E V S P T P P I T V T H K P E E D T F G V S I A

1321 GTTGGACTTCTGCTGTCTGTGTGCTGTCTTCTTCTGTCAATCATCAACAAATAATGTTGAGCGGTGCCAAATTTGCAATGAAGGTCCTGCGTGTGCTCATCTAGTGTGAGGAG  
405 Y G L A A F A C V L L Y V L F Y H I N K Y G R R S K F G H K G P V A V I S G E E

1441 GACTACAGCCAGCCACTGCAACCAATCAACAGGAGATCACAGCGCCTGTCTACTGTGATCCCGGCGCGAGACTGTGGTCAATGGATGCACTGGCAATCCCTGTCTCATTTAGMAACCCCGAG  
1445 D S A S P L H I N H G I T T P S S L D A G P D T V V I G H T T R I P V I E N P Q

[illegible]

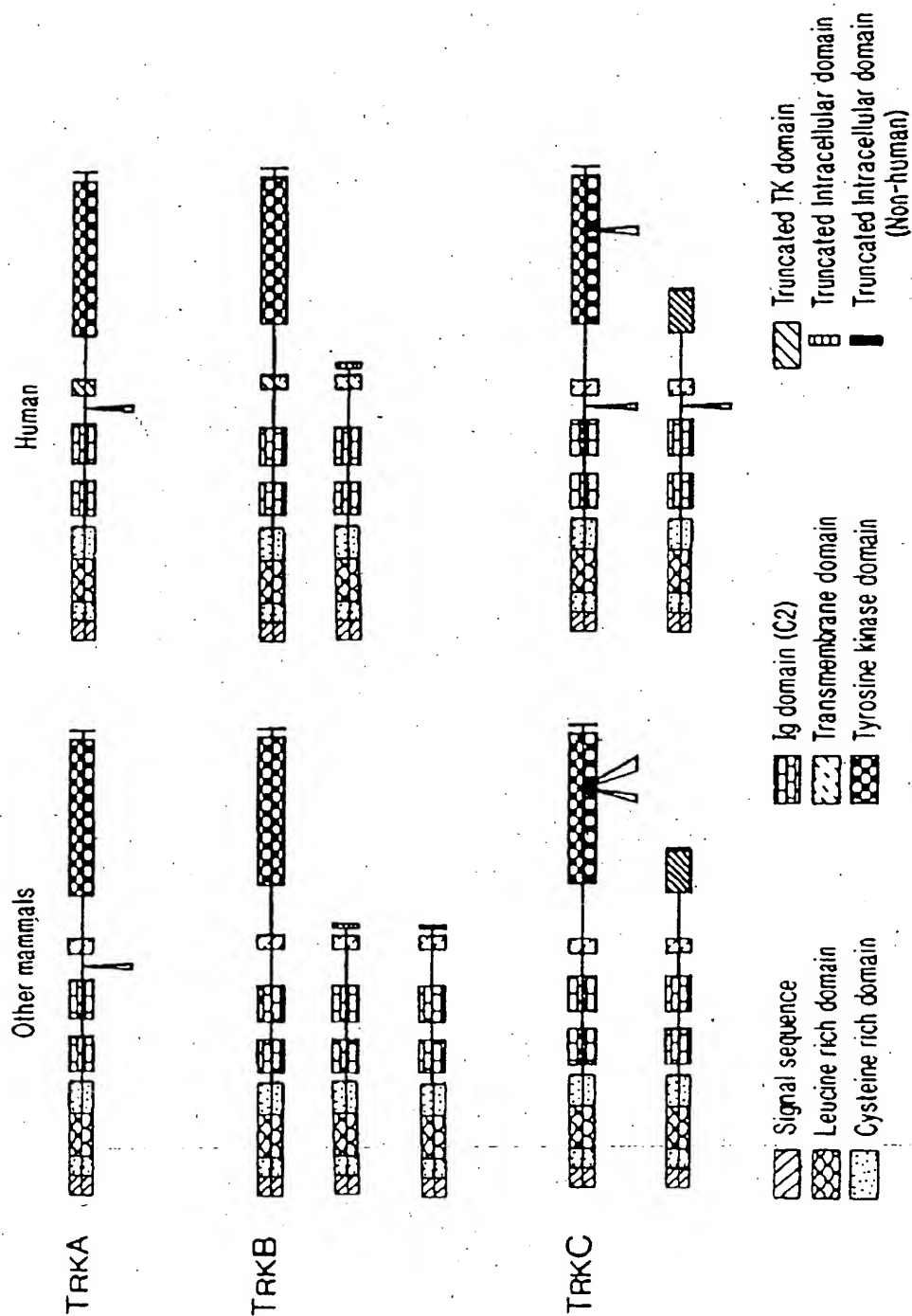


FIG. 4

Figure 1

[illegible]

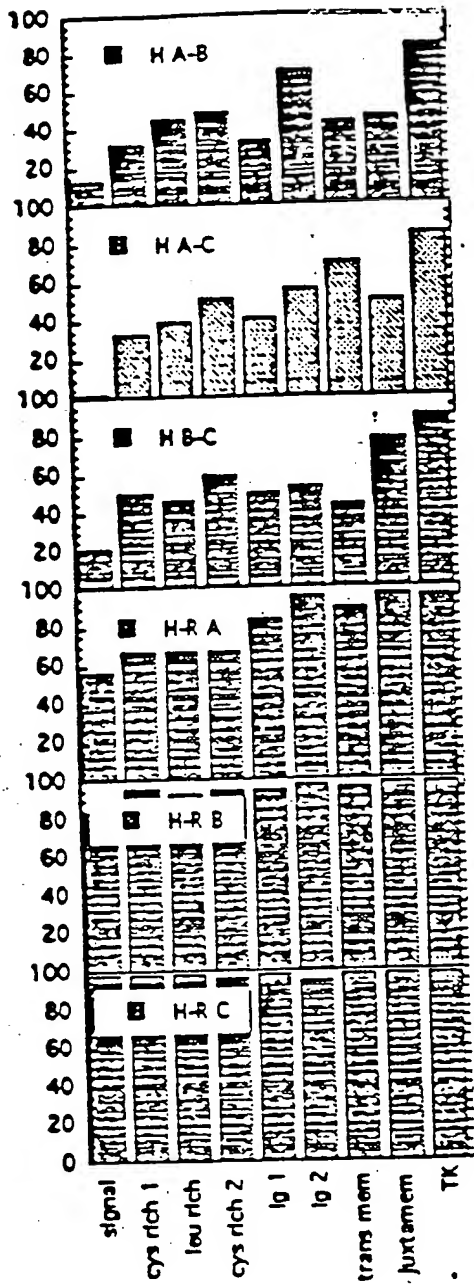


1590 TGGGCTCTTTCAACACAGACATCATGGATATTAAACTTCGAAGGACACAGAGATCATCTAATGCCATCACTCACTATATATACGAAGAACTCGAGGTCACAGACTGGGCAAGTGTCT  
498 M V F S M I D M M G I L N L K D M R D E L V P S T N T Y I Y E E P E V Q S G E V S

2710 TACTCAAGGTCACATGGTTTCACAGAAATTATGTTGAAATCGAATAAGGCTTCGGGACATTCGAAGCTCTTAAGCAATGCAATCTATGTTGACGATGTCGAATGTTTATTTCAAGCAAGGA  
538 Y P R S H G F R E I M L N P I S L P G N S E P L N M G I Y V E D V M V Y F S R G

1830 CCGCATGGCTTTTAAAAA  
578 R N G F O

Figure 3





Figur 4

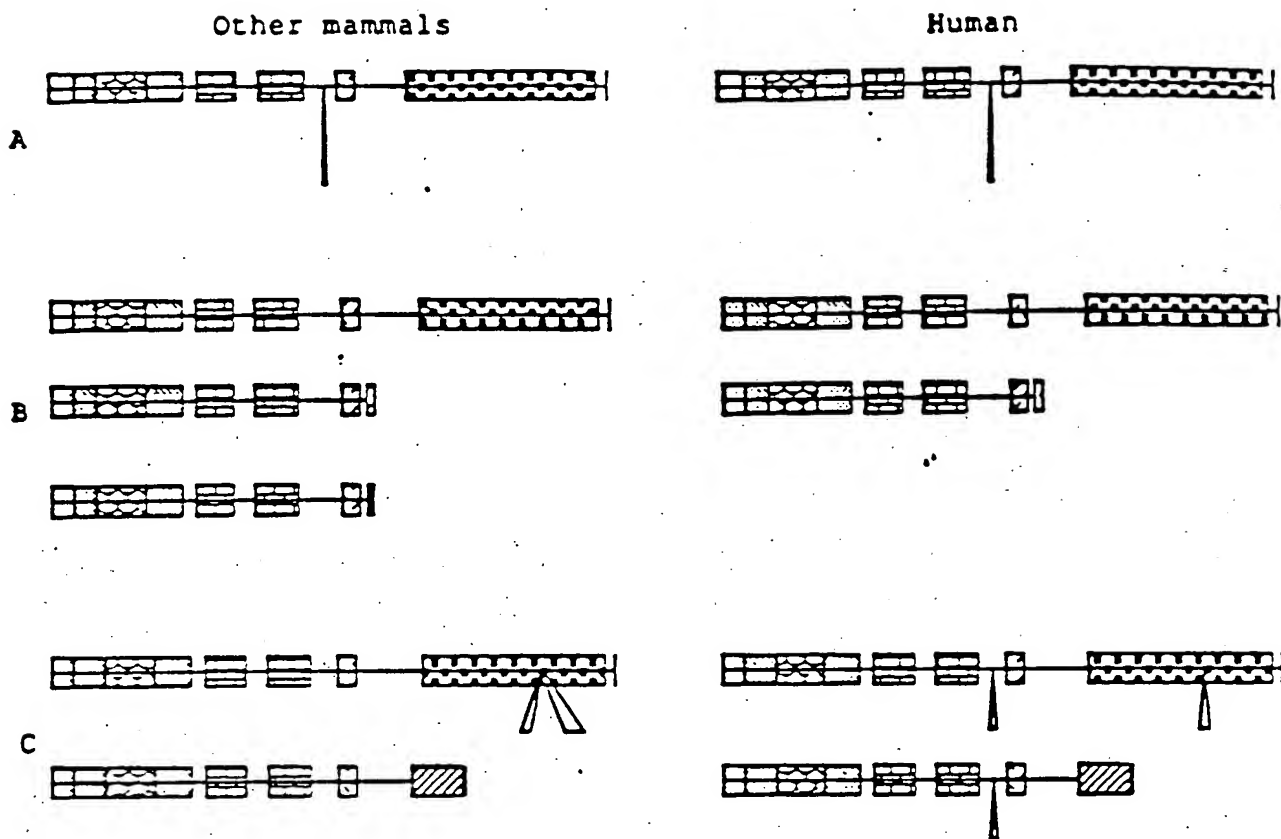


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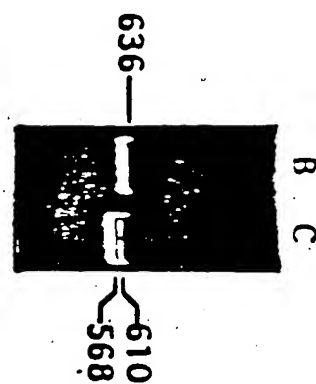


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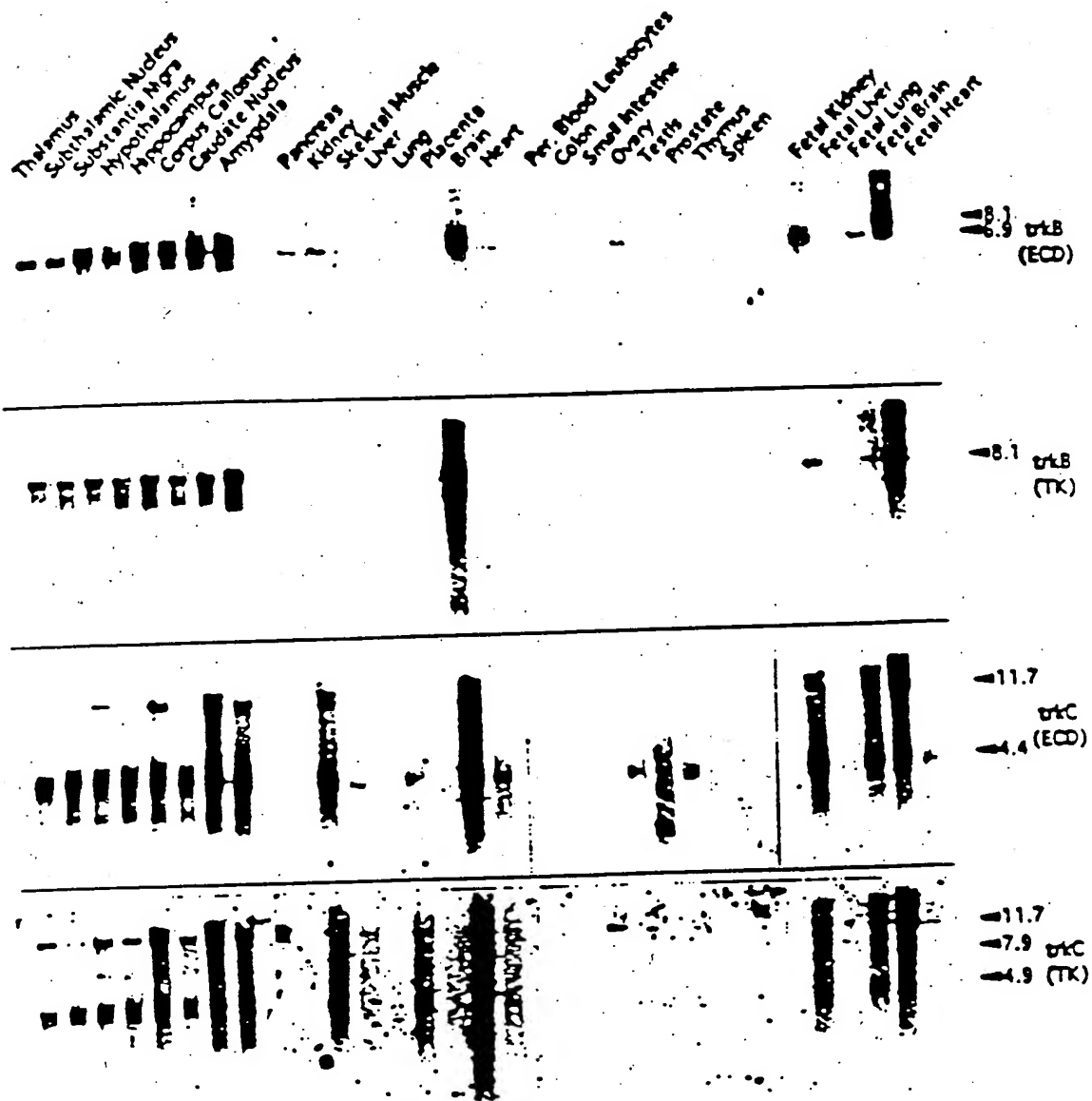
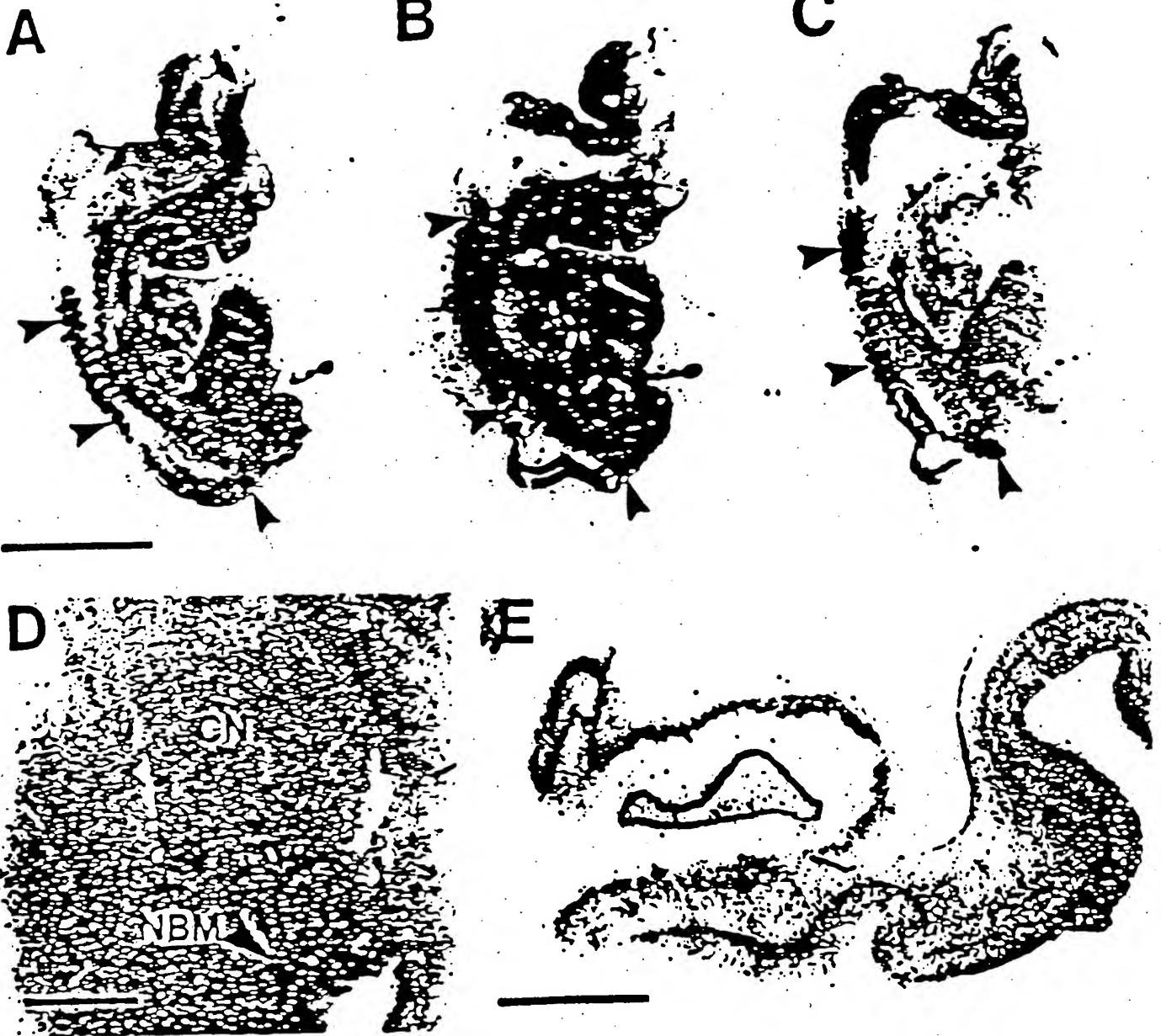


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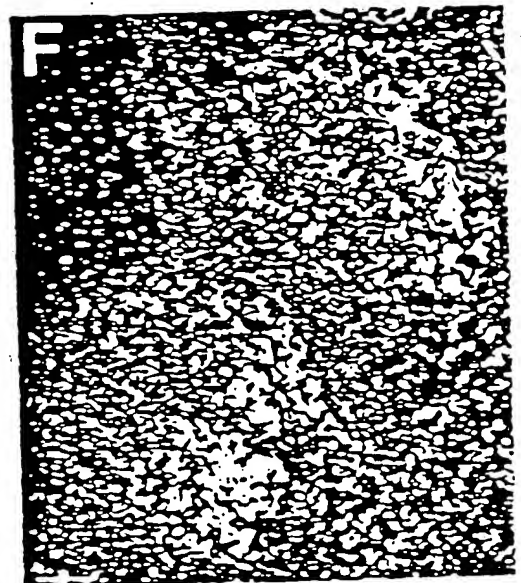
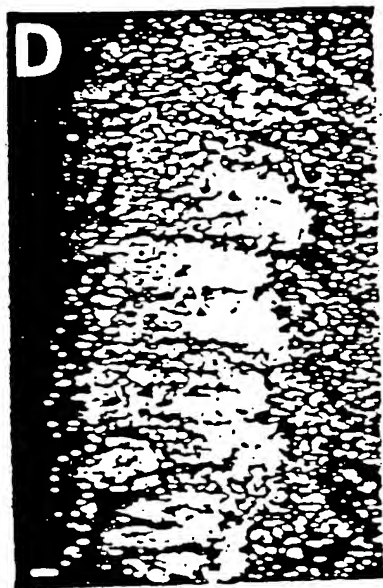
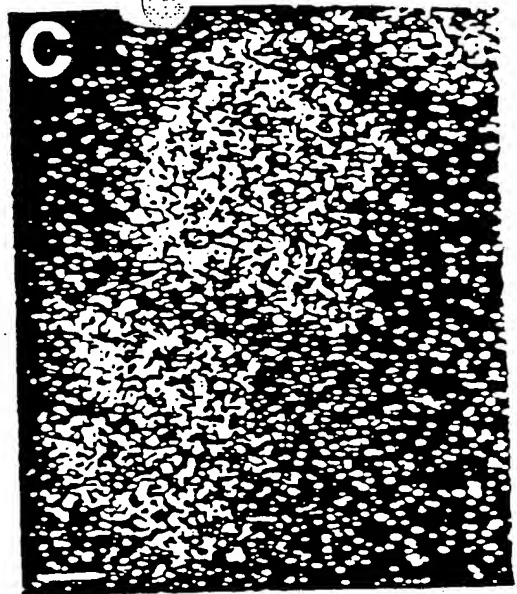
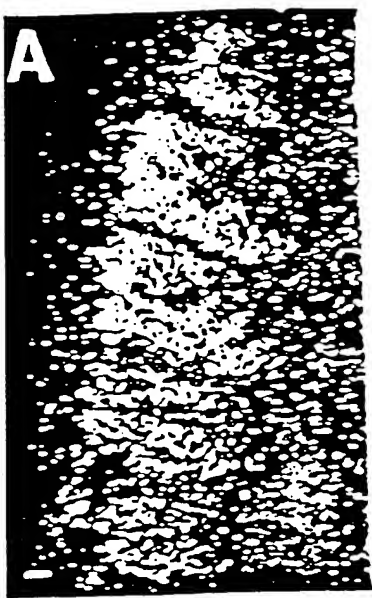


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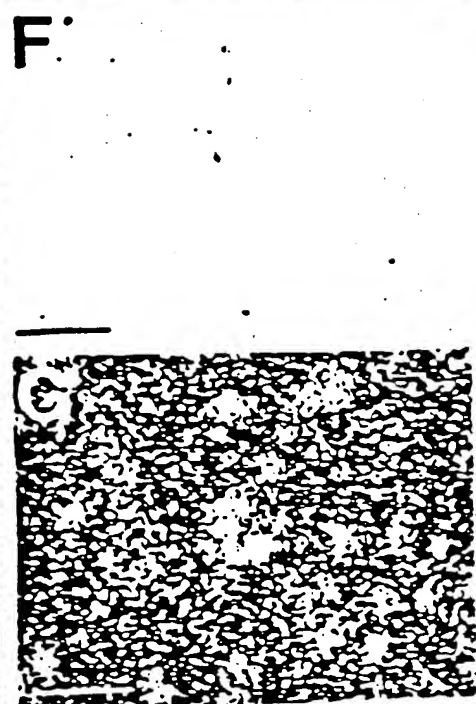
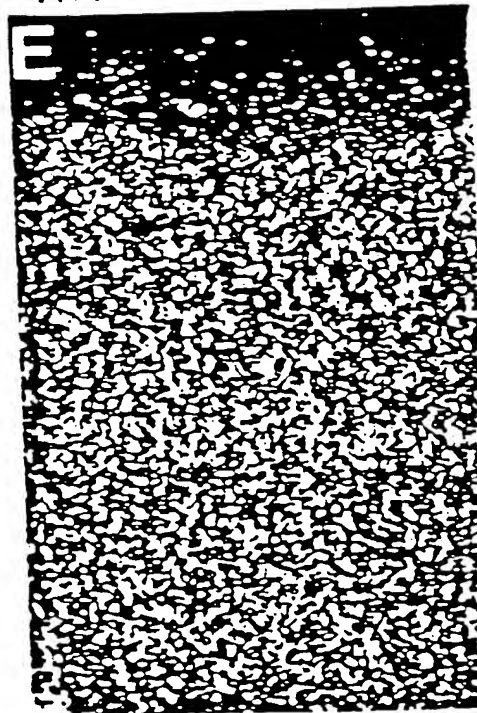
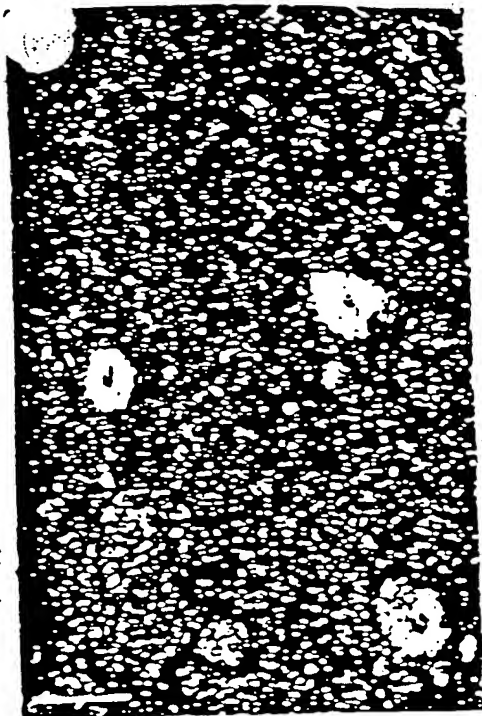
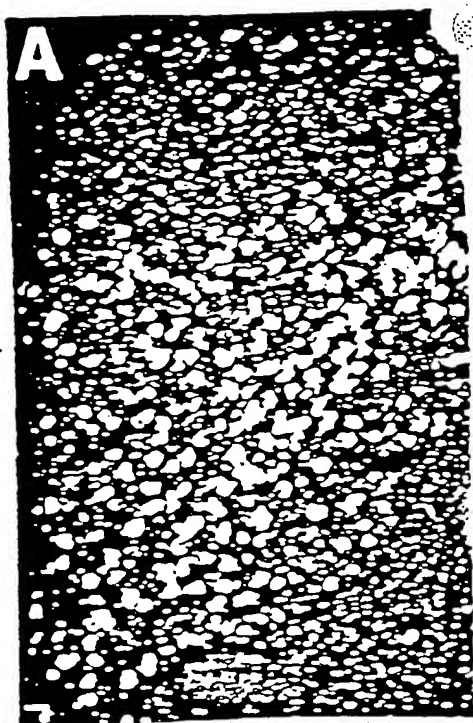


Figure 9

Figure 10

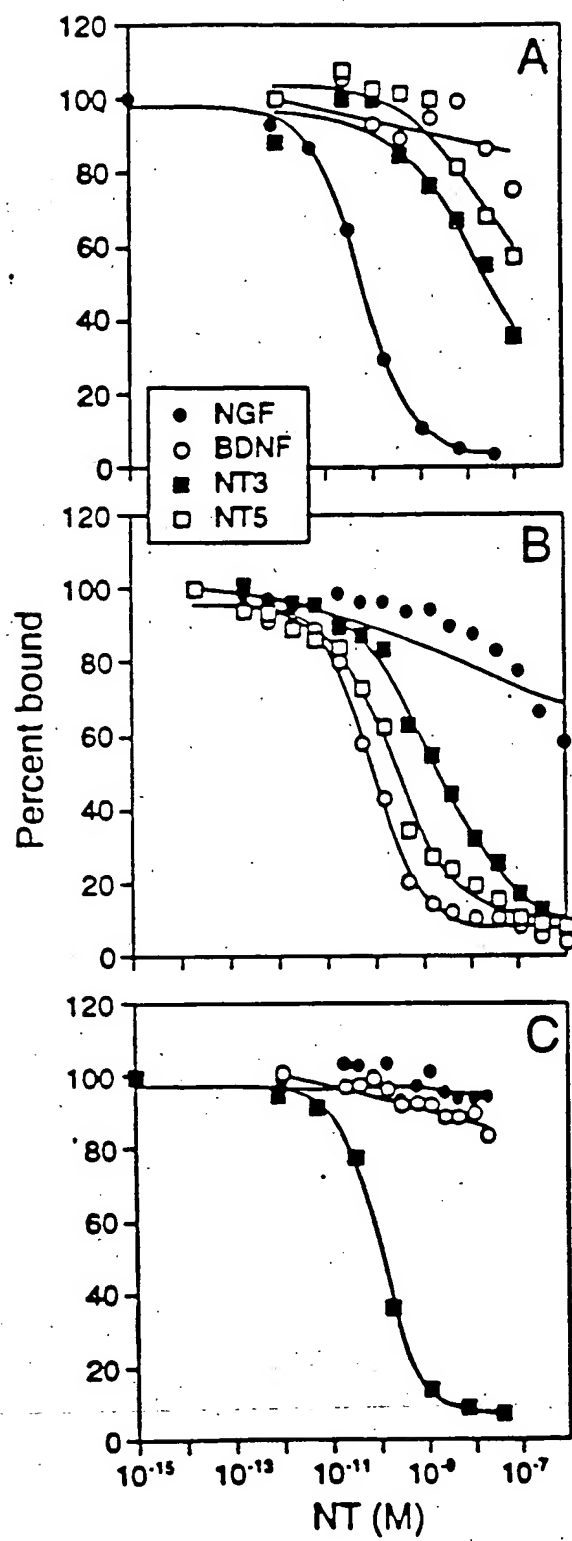


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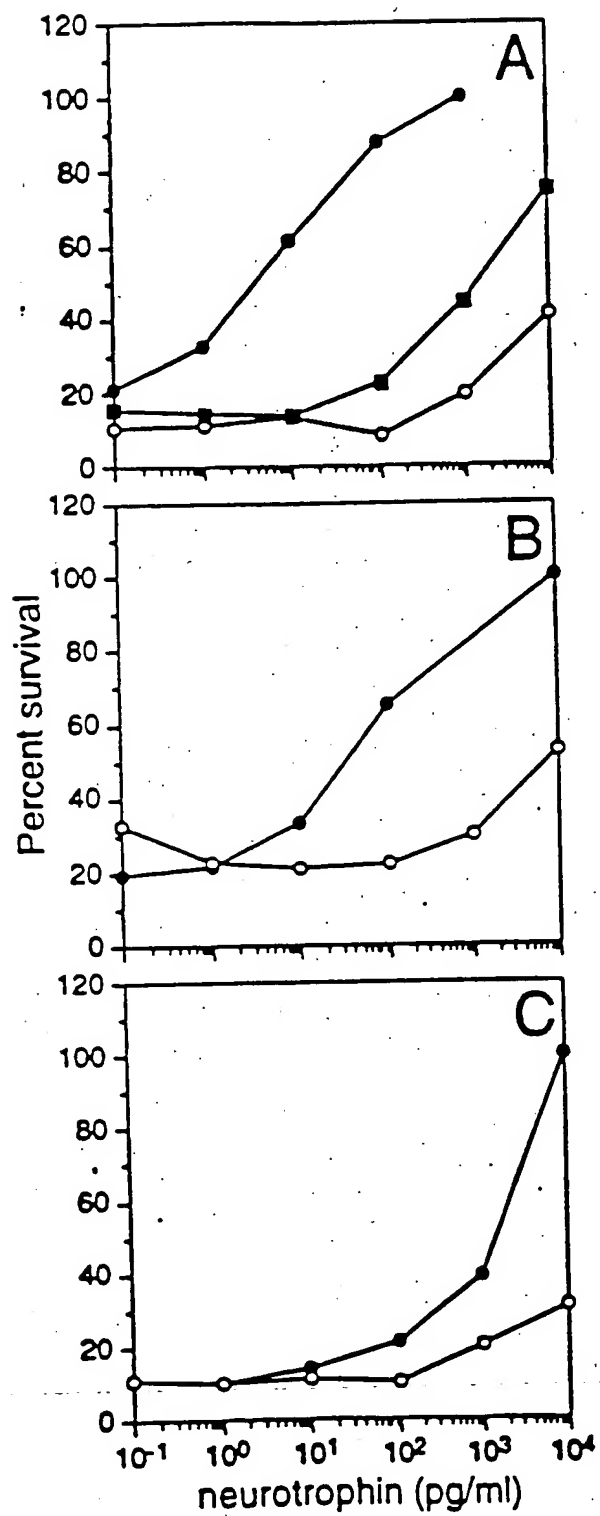




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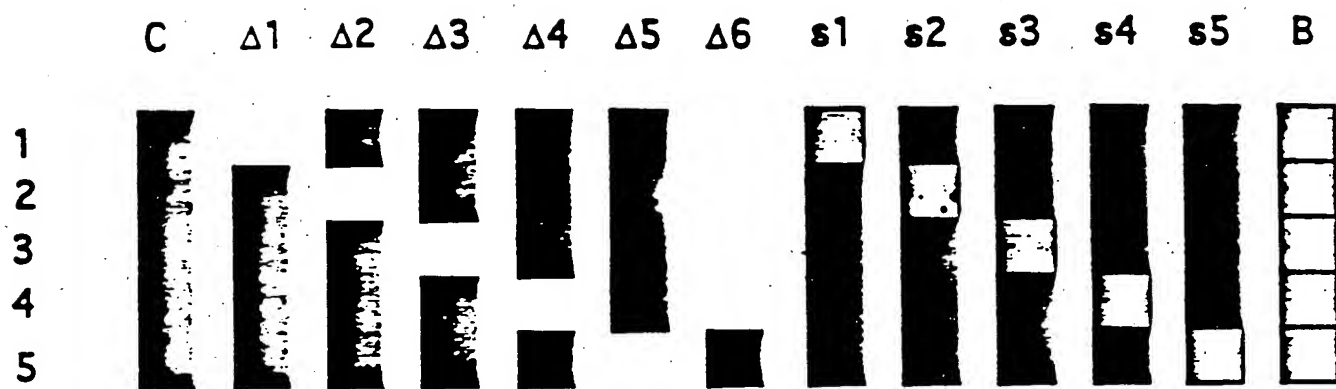


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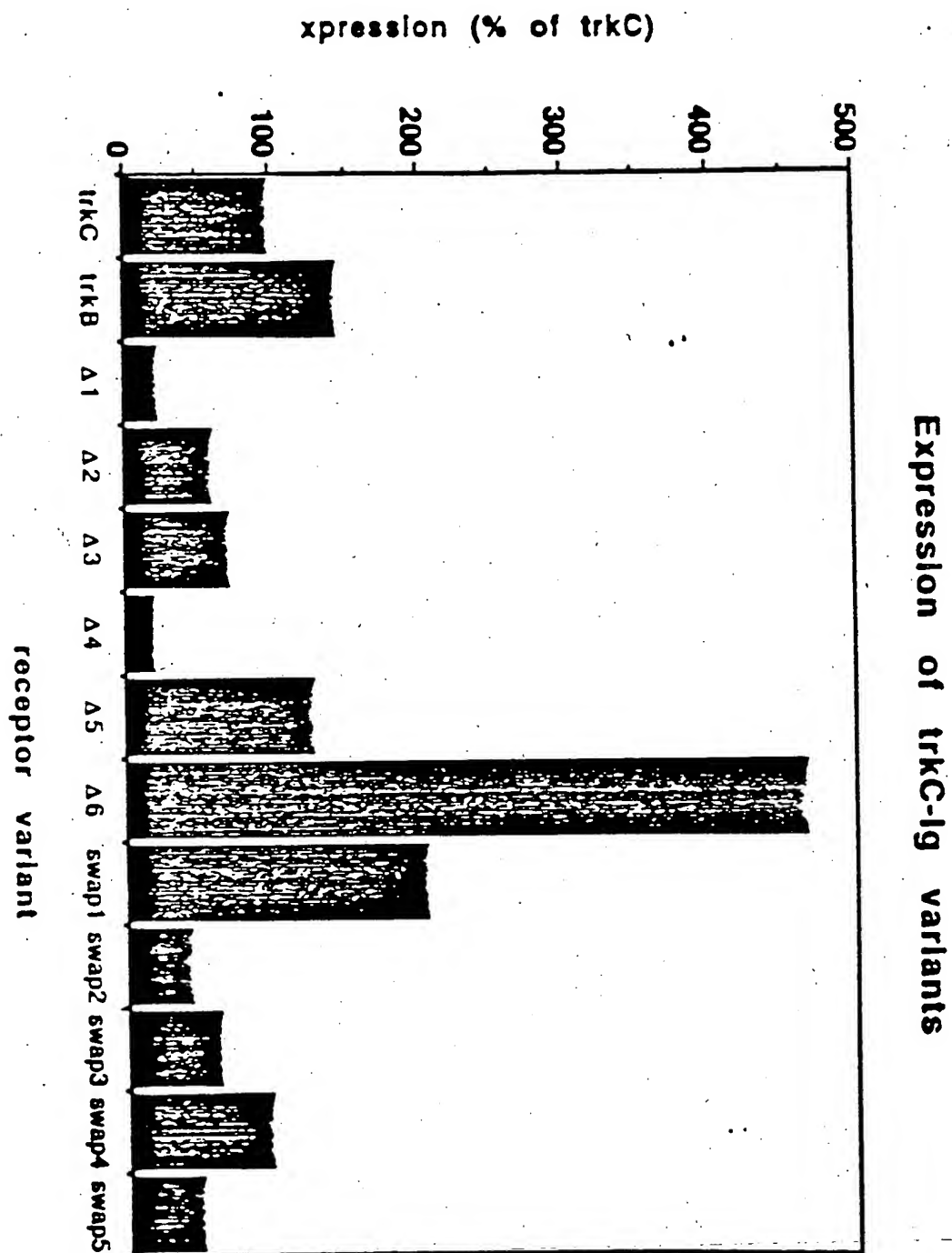


Figure 14A

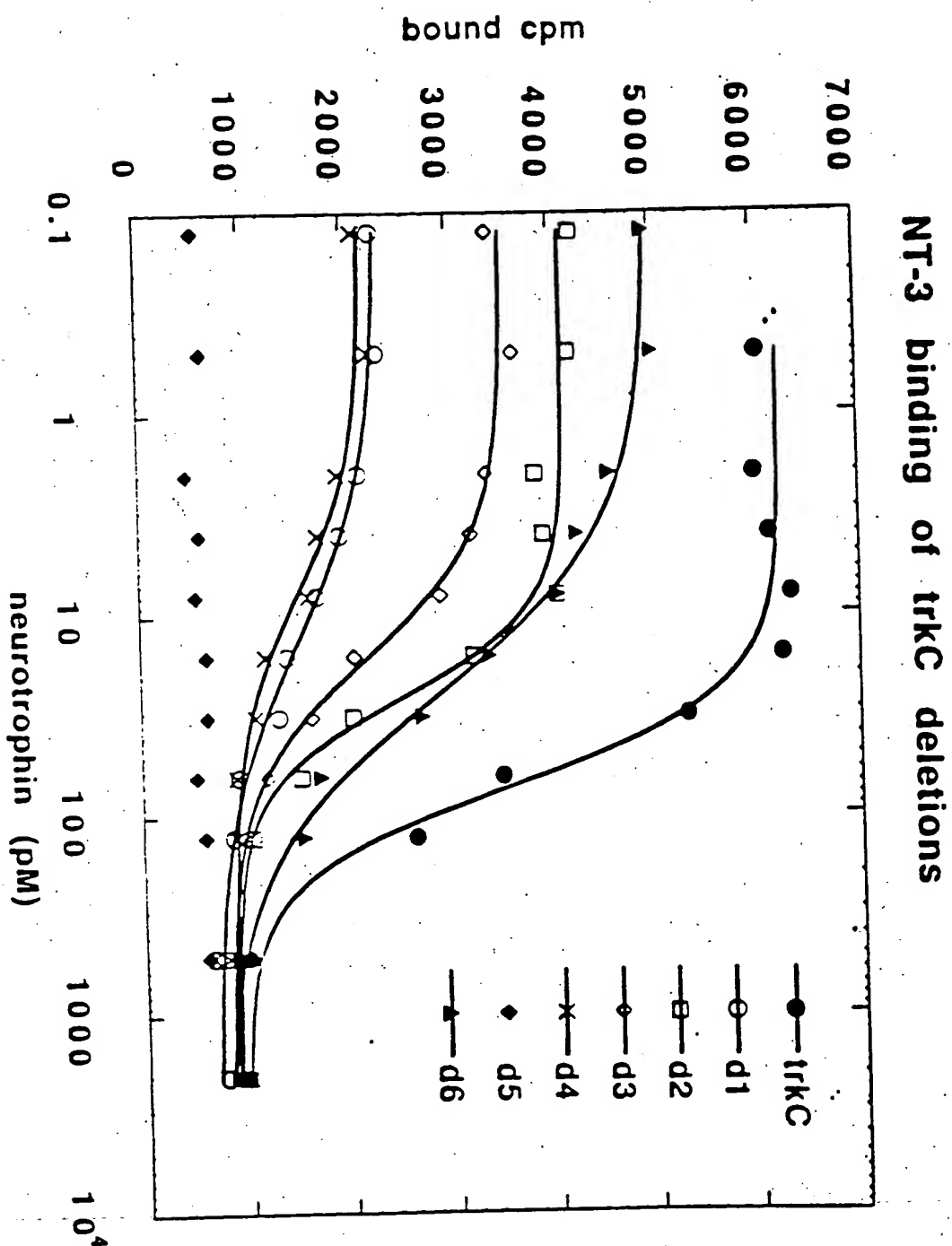


Figure 14B

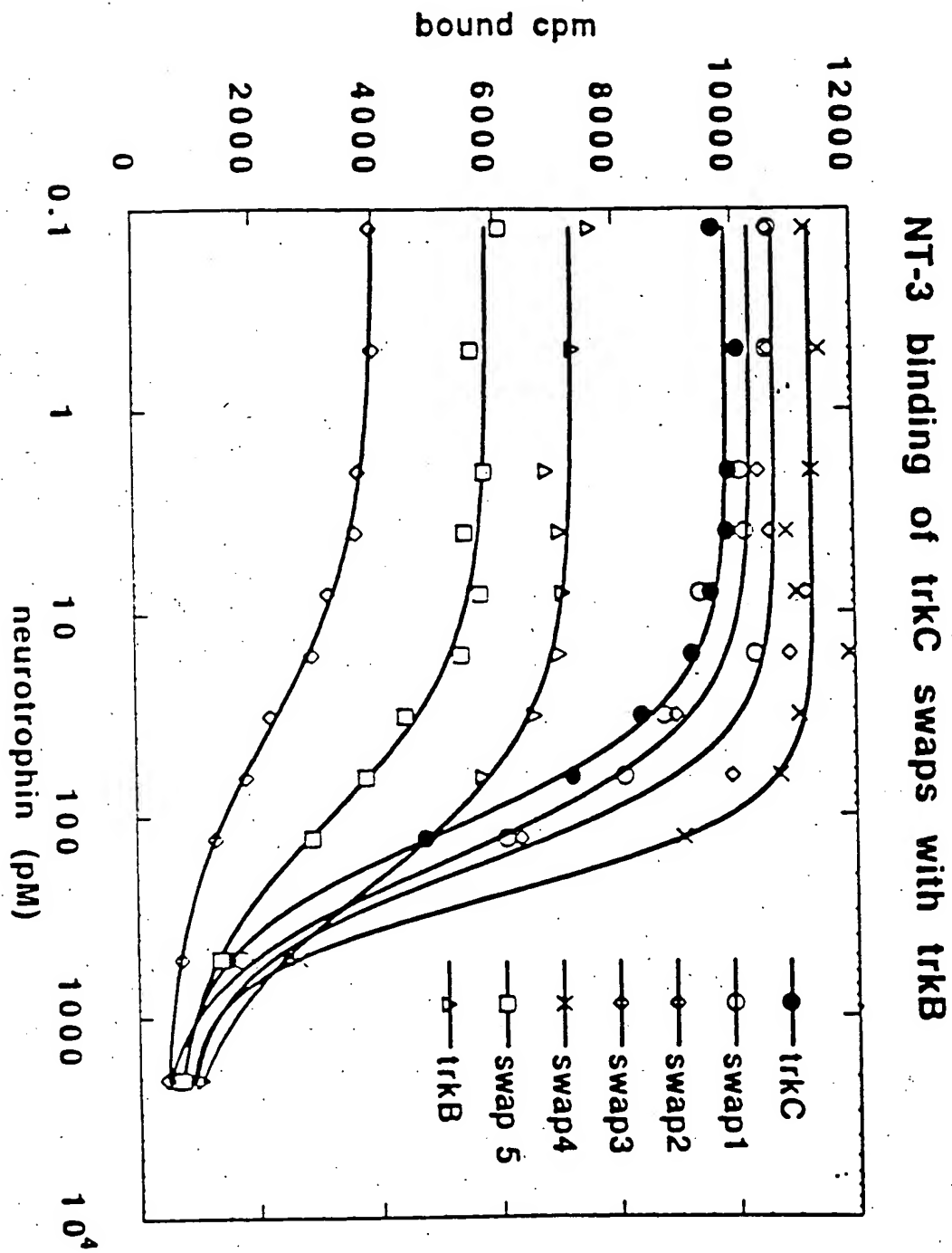
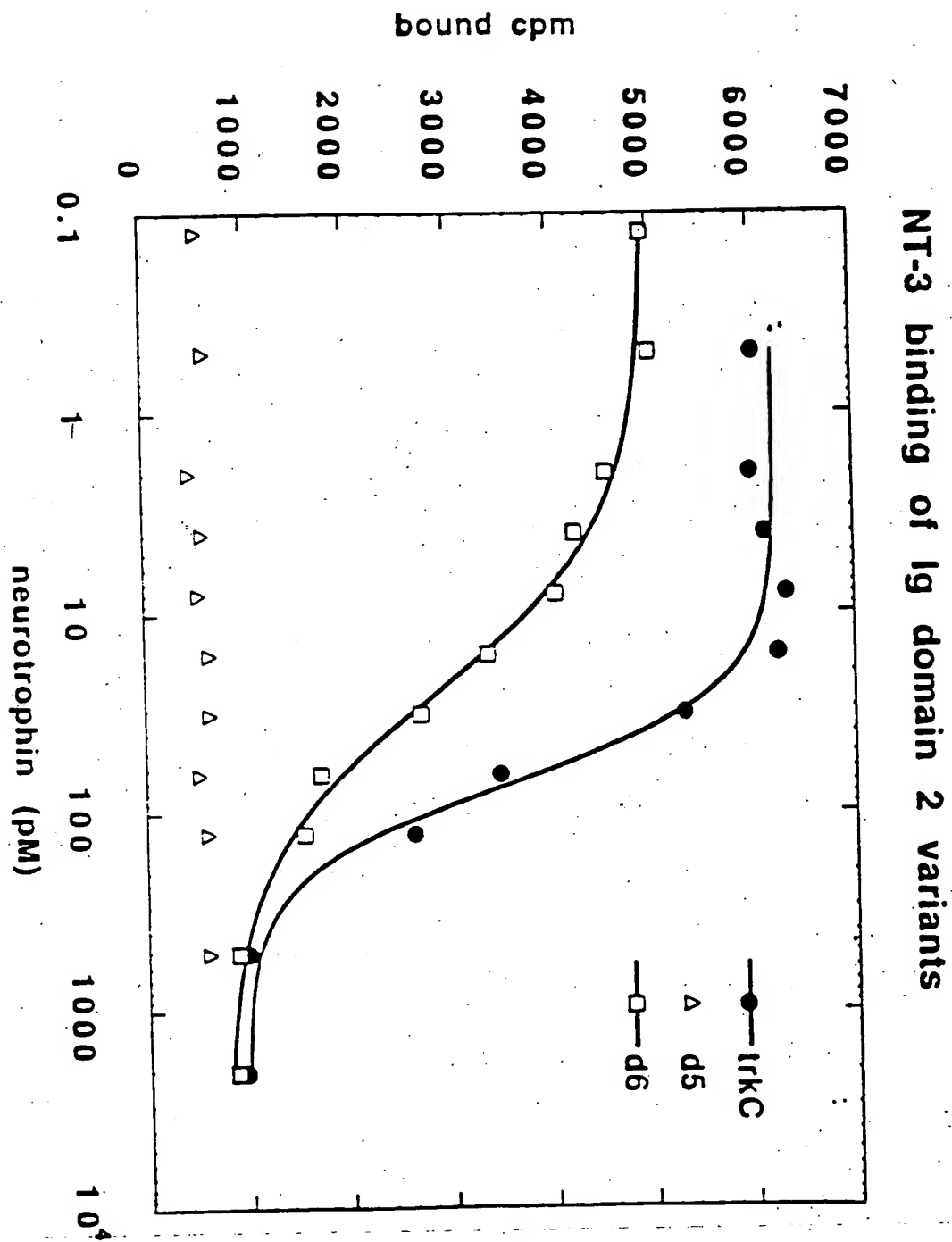


Figure 14C



## BDNF binding of deletions of trkB

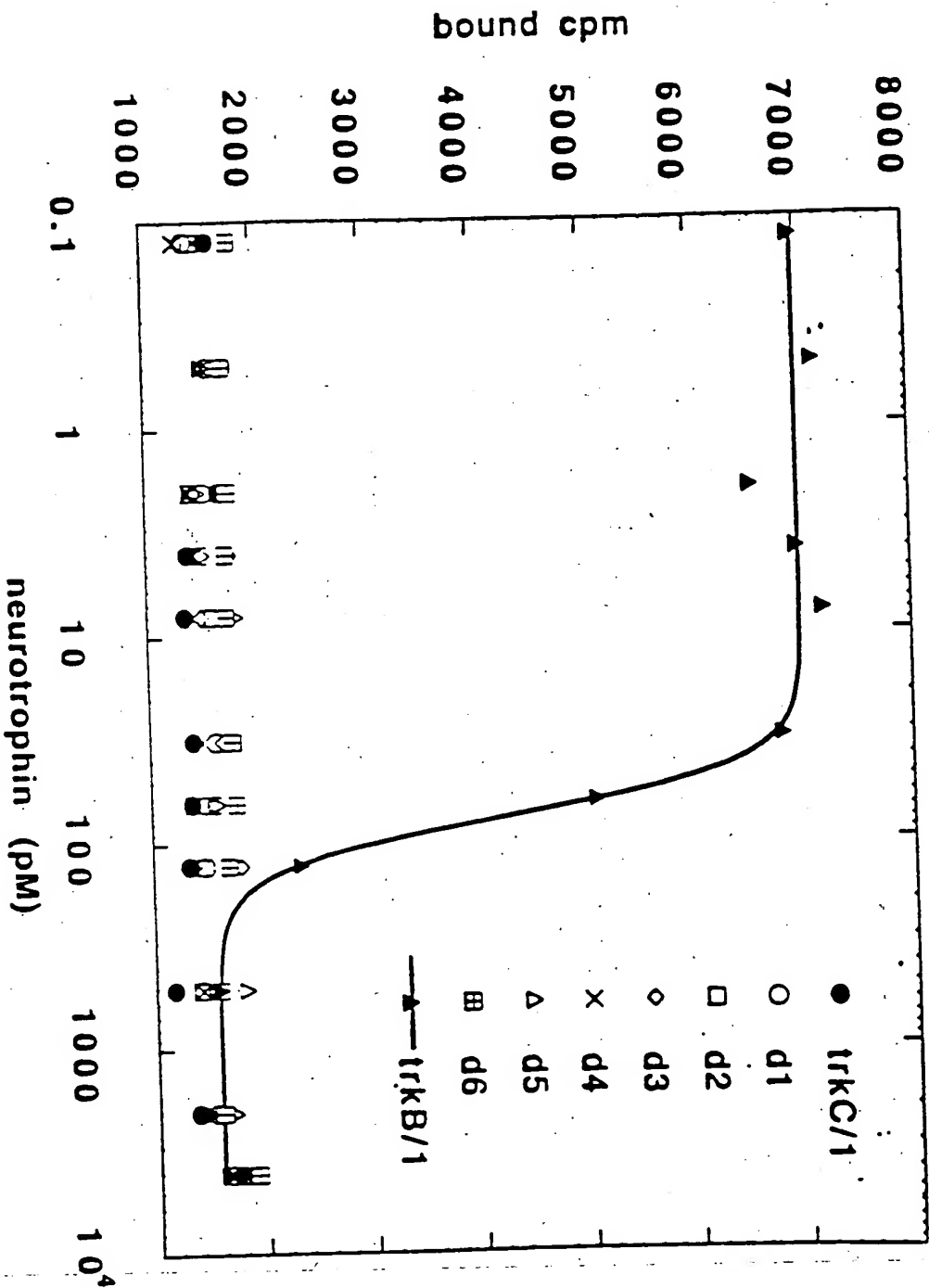


Figure 15B

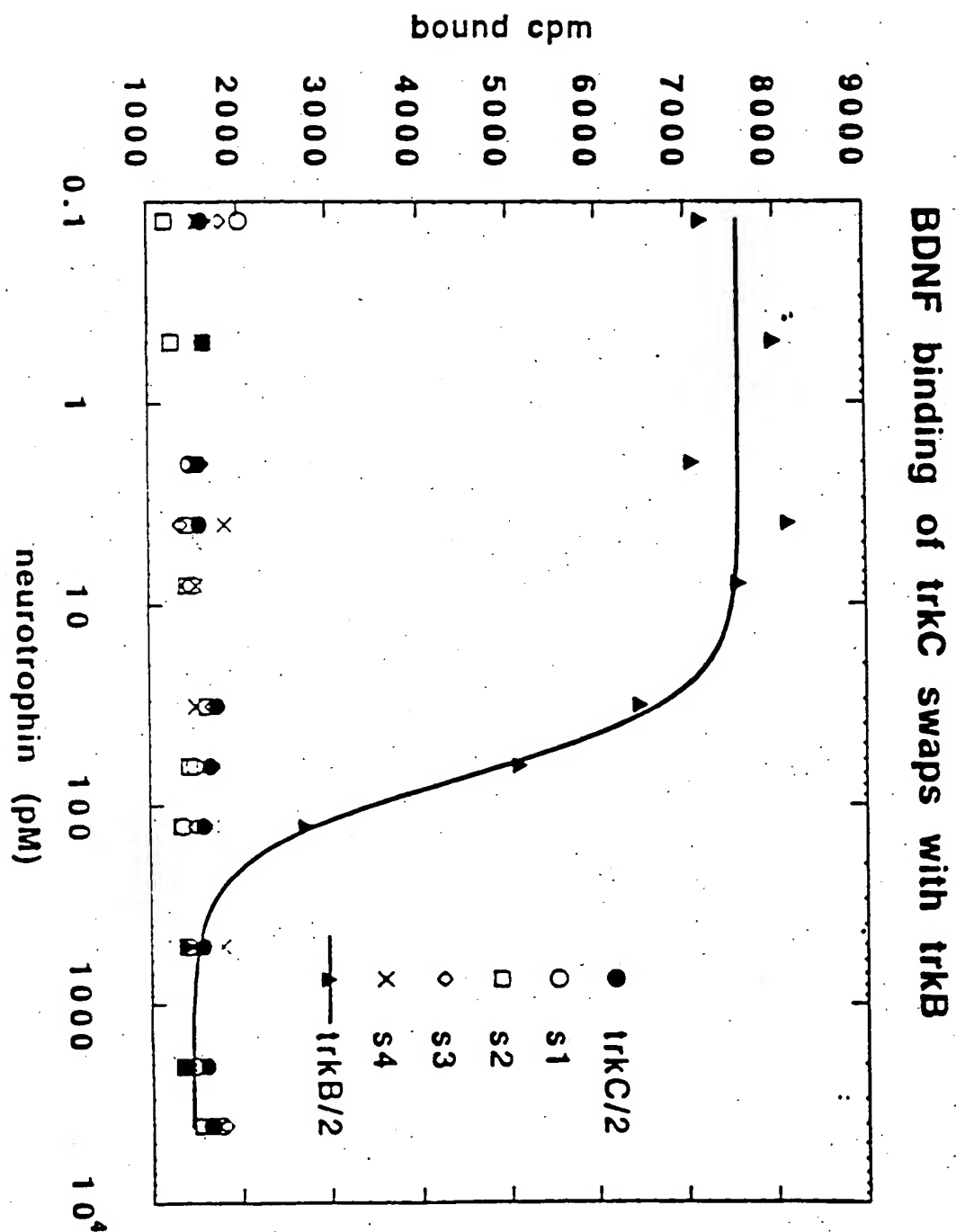
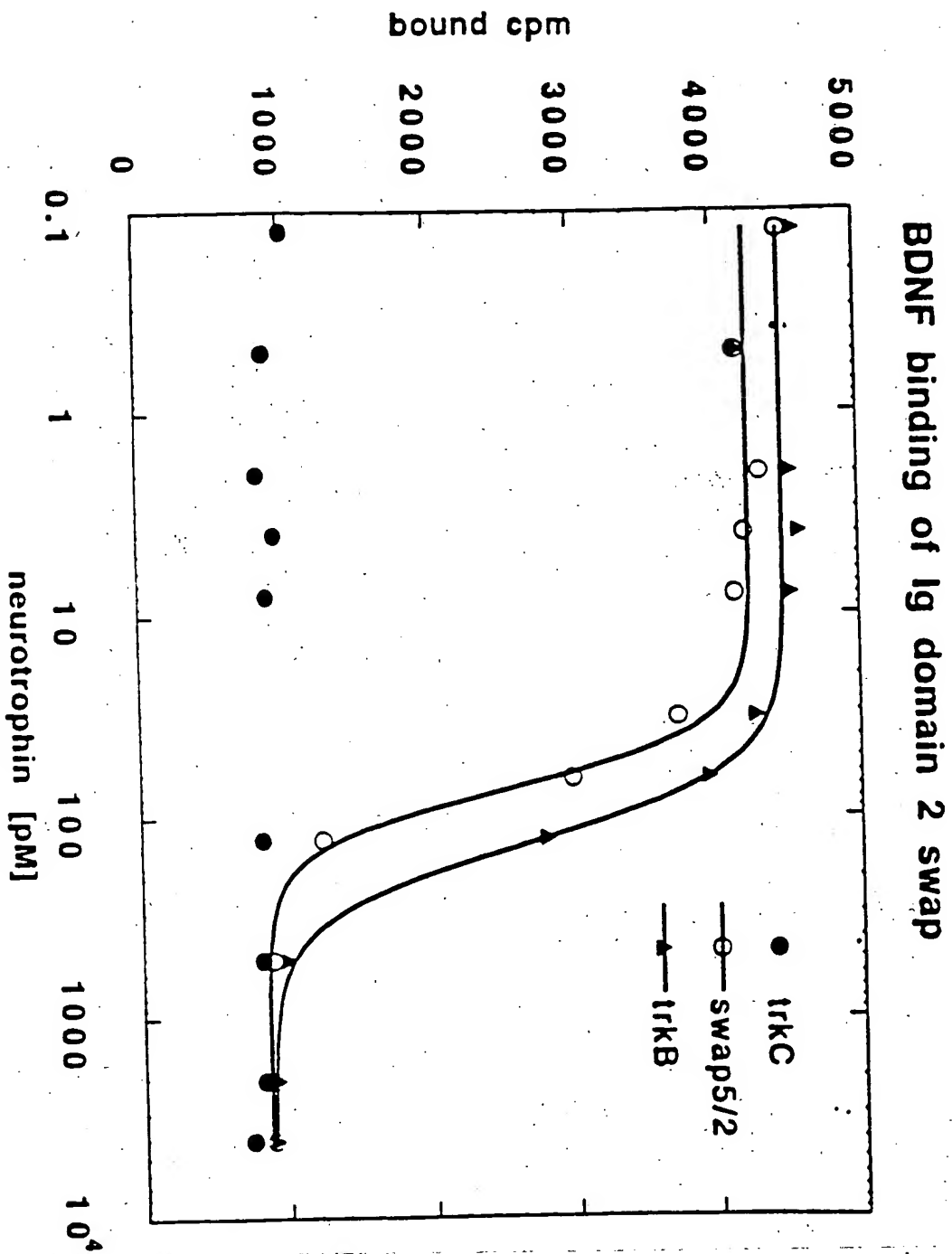


Figure 15C





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/-----Signal-----/-----Cysteine Rich 1-----/
trkA 1 MLRGGRRGQLGWSWAGPGSLLAWLILAS-----AGAAACPDACCPHGSSGLRCTR-DGALDSLHMLPG-----AENITELYIENOO
trkB 1 -----HSSWIRWHGPMARLWGFQNLVVGFW-----RAAFACPTS-CKCSASRIWCSDPSPGIVAFPRLEPNVD-----PENITEIFIANOK
trkC 1 -----MDVSL-----CPAKCSFWRI-FLLGSVWLDYVGSVLA-PAN-CVCSKTEINCRAPDDGNL-FPLLEGQDSQSNCHNANINITDISRMTSINIEWR

-----Leucine Rich-----/-----Cysteine
trkA 78 HLQHLRLRLRGLGELRNLTIVKSGLRFPVAPDAFHTFRLSRNLNLSFNALESLSWKTVQGLSLOELVLSGNPLWCSCLARMLQRNEEGLCGVPEOKLOC
trkB 78 RLEIINEDDVEAYVGLRNLTIVDSGLKFVANKAFKKNLNQHNFTRNKLTSLRKHFRHLDELILVGNPFTCSCDIMNITLQE-AKSSPDQDLYC
trkC 90 SLHTLNADVMEHYTGLQKLTIKNSGLRSIQPRAFAKNPHLRYNLSSNRLTTLWQLFOTLSLRELOLEONFFNCSCDIRNMQLMQEGEAKLNSQNYC

Rich II-----/-----Immunoglobulin I-----/
trkA 178 HGQG-----PLAMPHASCGPTLKVOVPNASVDVGDVLLRQVQEGRLQAGNLTLEQSATYMKSS-----GGLPSLGLTLANVTSDLRKNLTCAENL
trkB 177 LNESSKNIPLANIQIPNCGPSANLAAPNLVEEGKSLTSCSVACDPVPHMYWQGNLVSKHNNET-----SHTQG-SLRITNISDDSGKQISCVAEHL
trkC 190 INADGSQLPLFRHNI SQCDLPEISVSHVNLTVREGDNNAVITCMGSGSLPDVDNIYVTLQGISINTHQTNLWNTVHAINLTLVNVTSEDNGFTLTICIAENV

-----Immunoglobulin II-----/
trkA 271 VGRAEVSQVNVVSPASVO-LHTAVEMHH-CIPFSVDGQPAPSLRWLFNGSVLNETSFIETFELEPAANETVRHGCLRLNQPTVMNNGNYTLAANPFQO
trkB 272 VGEDQDSVNLTVHFAPTITFLSPSTDMH-CIPFTVKGNPKPALOWFYNGAILNESKYICTKIM--VTNHTIYHGCGLQDNPTMNNNGDYTLIAKNEYKG
trkC 290 VQMSNASVALTVYPPRVVSLEPELRLE-CIEFVVRGNPPPTLHWLWNGQPLRESKIHWETV--QGEIIS-EGCLLFNKPPTMYNNGNYTLIAKNP LGT

-----Transmembrane-----/
trkA 370 ASASIMAAFH-----DNPF-----EF-NPEDPIPDTS-----TSGDPVEKKDET-----FGVSVAVGLAVFACLFLLTLVIVKCGRRNKFGIN
trkB 370 DEKQISAHFMGWP GIDGAPNYPDVYIYEDYCTAANDIGDITNRSNEIPSTDVDTKTGREHLSVAVVVIASVVGFC-LLVHLFLL-KLARHSKFGHK
trkC 387 ANQTINGHFL-----KEPFEST-DNF-ILFDEVSPT-----PPIVTNHPFEED-----FGVSIAGVLAATACVLLVVLVFMH-KYGRRSKFGHK

-----Juxtamembrane-----/
trkA 446 RP-AVLAPEDGLAMS LHMFTLGSSSLSPTE-GKGSGLQG-----HIIENPOYF-----SDACVHHIKRDIVLKWLGEAGFGKVFLAECNHLPEQD
trkB 466 GPASVISNDDDSASPLHHISNGSNTPSSEGGPDVITGHTKIPVIENPOYFGITNSQLKPDITVQHIKRNIVLKLRELGEAGFGKVFLAECYNLCPEQD
trkC 466 GPVAVISGEEDSASPLHHINHGITTTPSSLDAGPDVTWIGHTRIPIENPOYFROGHNCHKPDITVQHIKRNIVLKLRELGEAGFGKVFLAECYNLSPTKD

-----Tyrosine Kinase-----/
trkA 532 KMLVAVKALKEASESARQDFQREAEILLTLQHQHIVRFFGVCTEGRPLLHVFEYMRNGDLNRFRLSHGPDAKLLAGGEDV-APGFLGLGQLLAVASQVAA
trkB 566 KILVAVKTLKQASDNARKQFHREAEILLTLQHEHIVKFGVCGVEGDLIMVFEYMKHGDINKFLRAHGPDVILMAEGNPP-----TELTSQMLHIAQQTAA
trkC 566 KMLVAVKALKOPTLAARKQFQREAEILLTLQHEHIVKFGVCGGQDPLIMVFEYMKHGDINKFLRAHGPDAMI LVDGQPRQAKGELGLSOMLHIASQIAS

-----/
trkA 631 GMVYLASQHFVHRDLATRNCLVGGGLVVKIGDFGMSRDVYSTDYRVGGRTMLPIRWMPPEISILYRKFTTESDVMSFGVVLWEIFTYQKOPWYQLSNTEA
trkB 663 GMVYLASQHFVHRDLATRNCLVGENLLVKIGDFGMSRDVYSTDYRVGGHTMLPIRWMPPEISIMYRKFTTESDVMSLGVVLWEIFTYQKOPWYQLSNNEV
trkC 666 GMVYLASQHFVHRDLATRNCLVGANLLVKIGDFGMSRDVYSTDYRVGGHTMLPIRWMPPEISIMYRKFTTESDVMSFGVILWEIFTYQKOPWYQLSNTEV

-----/
trkA 731 IDGITQGRELERPRACPEVYAIMRGCWQREPQORHSIKDVHARLOALACAPPVYLQVLG
trkB 763 IECITQGRVLRAPRTCPQEVYELMLGCWQREPMMKNIKSIHTLLONLAKASPVYLDILG
trkC 780 IECITQGRVLERPRVCFKEVYDVMLGWQREPQORLNKEIKILNALCATPPIYLDILG

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Figure 16

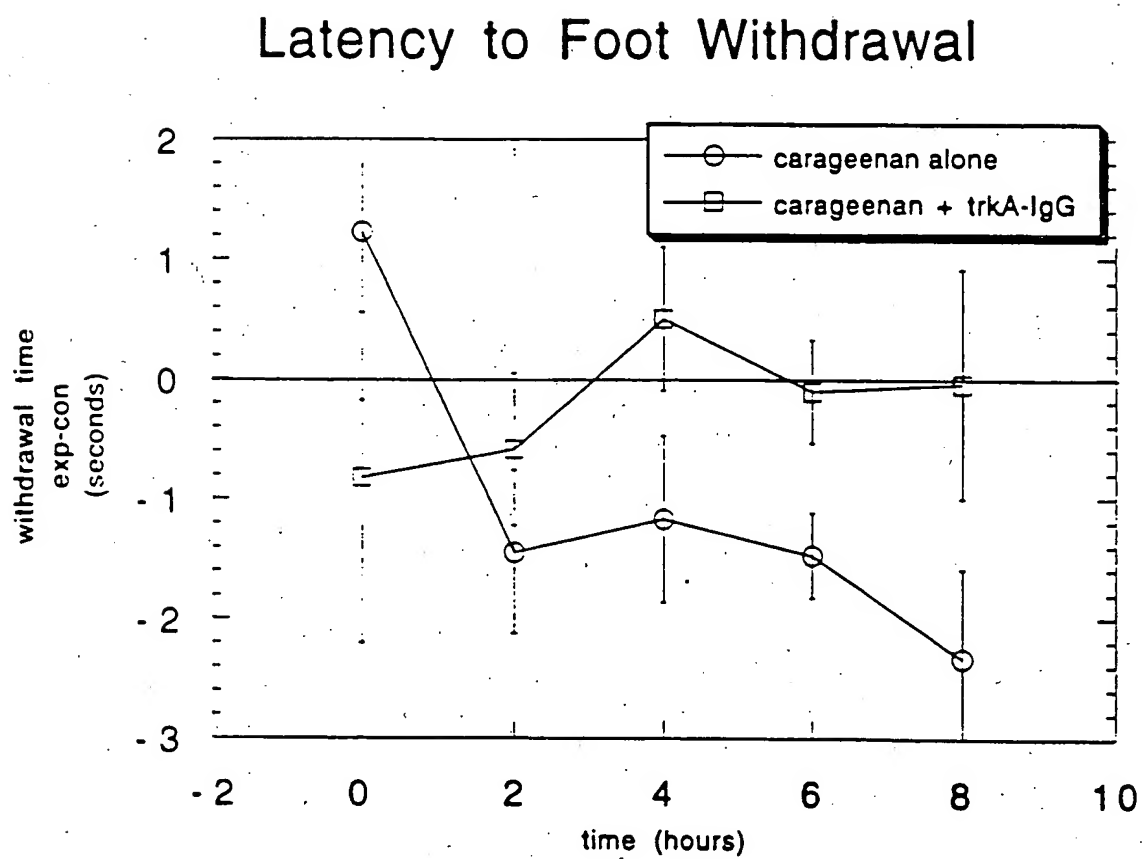


Figure 17

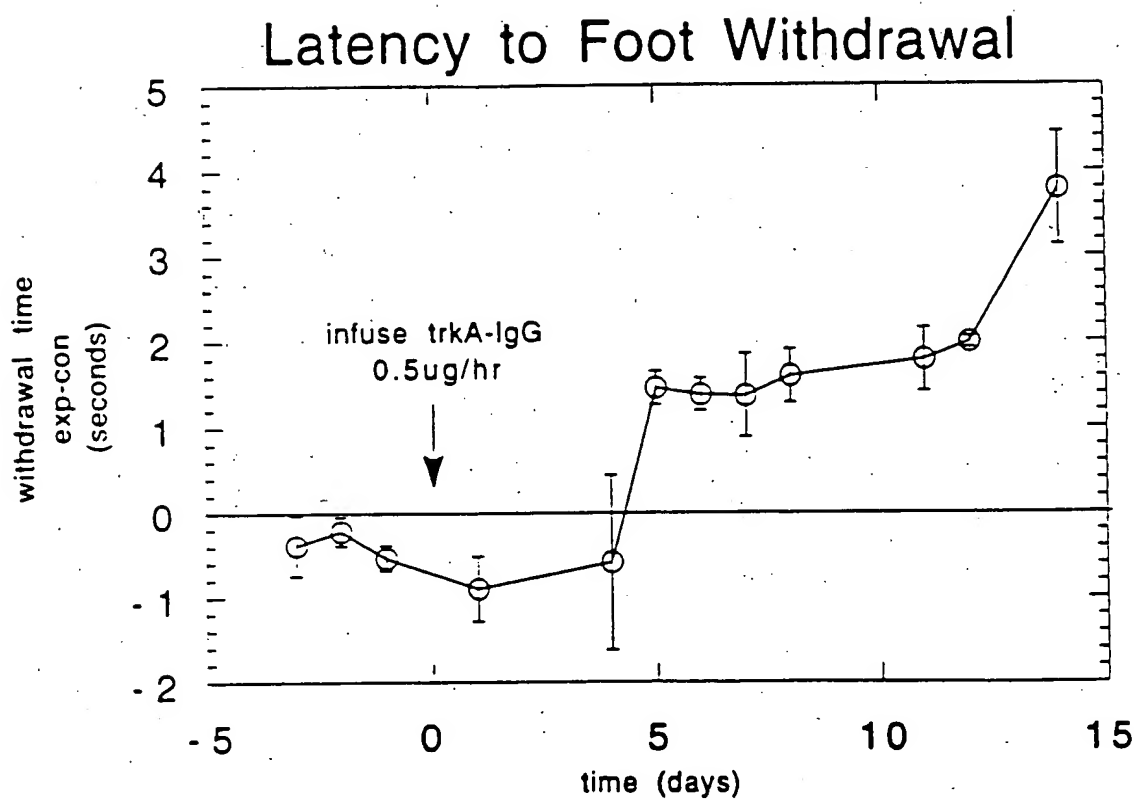


Figure 18